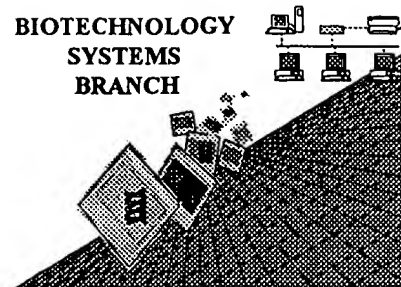


n/a

RAW SEQUENCE LISTING ERROR REPORT

#5
BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/423,545

Art Unit / Team No. : 1646

Date Processed by STIC: 2/28/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

RECEIVED
MAR - 9 2000
TC 1600 MAIL ROOM

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/423,545

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 **Variable Length** Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 **Skipped Sequences (OLD RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 **Skipped Sequences (NEW RULES)** Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 **Use of <213>Organism (NEW RULES)** Sequence(s) are missing this mandatory field or its response.
- 12 **Use of <220>Feature (NEW RULES)** Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RECEIVED
 MAR - 9 2000
 TC 1600 MAIL ROOM

NA

1646

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545DATE: 02/28/2000
TIME: 16:34:20

Input Set: I423545.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1 <110> Kenji SHIBATA
2 Motoo YAMASAKI
3 Tetsuo YOSHIDA
4 Tamio MIZUKAMI
5 Akeo SHINKAI
6 Hideharu ANAZAWA
7 <120> Peptides having a cyclic structure and restoring the
8 activities of P53 protein to mutant P53 protein
9 <130> 1061
10 <140> US/09/423,545
11 <141> 1999-11-12
12 <150> JP97/126113
13 <151> 1997-05-15
14 <160> 32

ERRORED SEQUENCES FOLLOW

E--> 15 <210> 8
16 <211> 32
17 <212> DNA
18 <213> Artificial Sequence
19 <220>
20 <223> Other nucleic acid Synthetic DNA
21 <400> 8
E--> 22 CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
23 32

under new sequence (see item 1 on Error Summary sheet)
Rules, all bases
need to be in lower-case
format error
↓ letters

E--> 24 <210> 9
25 <211> 32
26 <212> DNA
27 <213> Artificial Sequence
28 <220>
29 <223> Other nucleic acid Synthetic DNA
30 <400> 9
E--> 31 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
32 32

E--> 33 <210> 10
34 <211> 26
35 <212> DNA
36 <213> Artificial Sequence
37 <220>

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545DATE: 02/28/2000
TIME: 16:34:20

Input Set: I423545.RAW

38 <223> Other nucleic acid Synthetic DNA
39 <400> 10
E--> 40 TCGAGAGACA TGCCTAGACA TGCCTG
41 26

42 <210> 11
E--> 43 <211> 26
44 <212> DNA
45 <213> Artificial Sequence
46 <220>
47 <223> Other nucleic acid Synthetic DNA
48 <400> 11
E--> 49 TCGACAGGCA TGTCTAGGCA TGTCTC
50 26

51 <210> 12
E--> 52 <211> 22
53 <212> DNA
54 <213> Artificial Sequence
55 <220>
56 <223> Other nucleic acid Synthetic DNA
57 <400> 12
E--> 58 TCGAGCCCGG GGGTACCGCA TG
59 22

60 <210> 13
E--> 61 <211> 14
62 <212> DNA
63 <213> Artificial Sequence
64 <220>
65 <223> Other nucleic acid Synthetic DNA
66 <400> 13
E--> 67 CGGTACCCCC GGGC
68 14

69 <210> 14
E--> 70 <211> 32
71 <212> DNA
72 <213> Artificial Sequence
73 <220>
74 <223> Other nucleic acid Synthetic DNA
75 <400> 14
E--> 76 TCGAGGGACT TGCCTGGACT TGCCTGTCTGA CG
77 32

78 <210> 15
E--> 79 <211> 32
80 <212> DNA
81 <213> Artificial Sequence
82 <220>

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545

DATE: 02/28/2000
TIME: 16:34:20

Input Set: I423545.RAW

83 <223> Other nucleic acid Synthetic DNA
84 <400> 15
E--> 85 GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
86 32

E--> 87 <210> 24
88 <211> (16) 15 shown
89 <212> PRT
90 <213> Artificial Sequence
91 <220>
92 <221> BINDING
93 <222> (7)..(13)
94 <223> BINDING type is -CONH2-.
95 <220>
96 <221> SITE
97 <222> (15)
98 <223> Xaa represents L-Leucine amide.
99 <220>
100 <223> Synthetic peptide
101 <400> 24
W--> 102 Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser Arg His Lys Lys Xaa
103 1 5 10- 15-

raw amino acid
numbers directly
under pertinent amino
acid. DO NOT use TAB
codes between numbers; use
space characters.

PRT
↓

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I423545.RAW

Line	Error/Warning	Original Text
16	E Input 32, Calc# Bases 0 differ	<211> 32
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
25	E Input 32, Calc# Bases 0 differ	<211> 32
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
34	E Input 26, Calc# Bases 0 differ	<211> 26
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
43	E Input 26, Calc# Bases 0 differ	<211> 26
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
52	E Input 22, Calc# Bases 0 differ	<211> 22
58	E Wrong Amino Acid Designator	TCGAGCCCGG GGGTACCGCA TG
58	E Wrong Amino Acid Designator	TCGAGCCCGG GGGTACCGCA TG
58	E Wrong Amino Acid Designator	TCGAGCCCGG GGGTACCGCA TG
61	E Input 14, Calc# Bases 0 differ	<211> 14
67	E Wrong Amino Acid Designator	CGGTACCCCC GGGC
67	E Wrong Amino Acid Designator	CGGTACCCCC GGGC
70	E Input 32, Calc# Bases 0 differ	<211> 32
76	E Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCCTGTCTGA CG
76	E Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCCTGTCTGA CG
76	E Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCCTGTCTGA CG
76	E Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCCTGTCTGA CG
79	E Input 32, Calc# Bases 0 differ	<211> 32
85	E Wrong Amino Acid Designator	GTACCGTCTGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCTGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCTGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCTGA CAGGCAAGTC CAGGCAAGTC CC
88	E Input 16, Calc Seq.Length 15 differ	<211> 16
102	W "N" or "Xaa" used: Feature required	Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser A